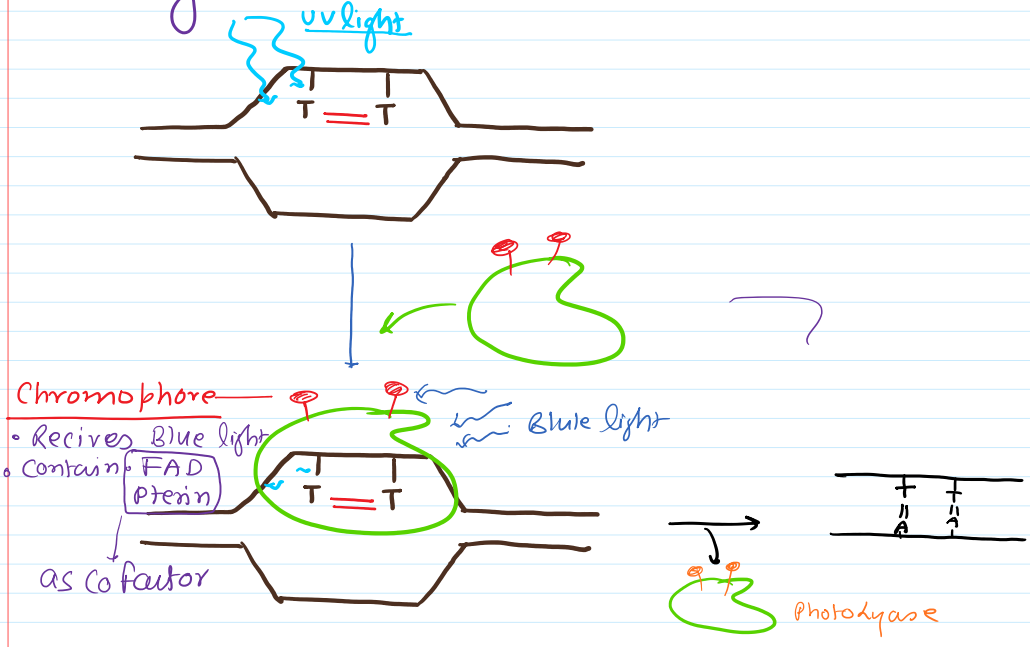
Direct Repair

① Photolyase

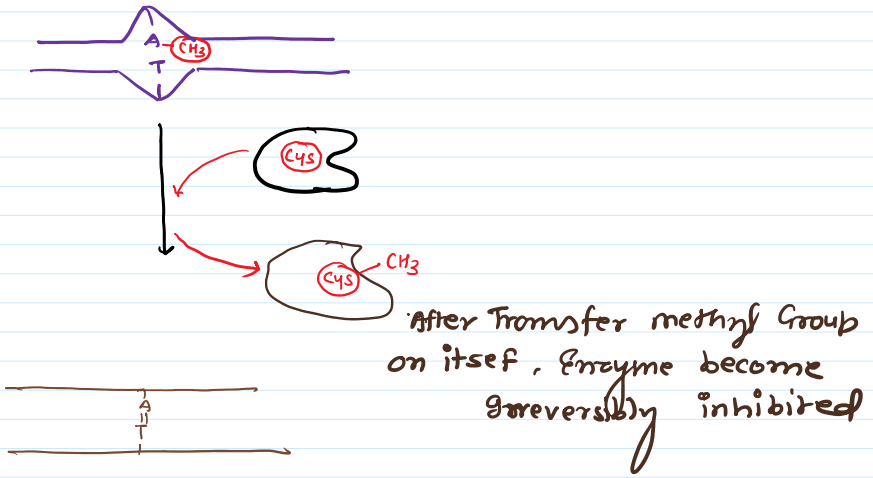
- involve in Direct Repair
- By photoactivation mechanism



→ When Chromophore recives Blue light Photolyase Become active & Resolve the Cyclobutane ring

ii Alkyle Transferase / methyl Transferase

↳ Suicidal Enzyme works in Direct repair



After Transfer methyl Group on itself, Enzyme become Irreversibly inhibited

② Excision Repair

✓ ① Mismatch Repair

→ Global Nt Excision ✓

① Mismatch Repair

② Nt Excision Repair → Global Nt Excision
→ Transcription Coupled Repair

③ Base Excision Repair

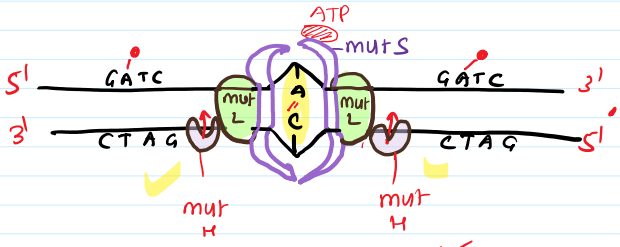
① Mismatch Repair

- Replication Coupled Repair mechanism in E. coli

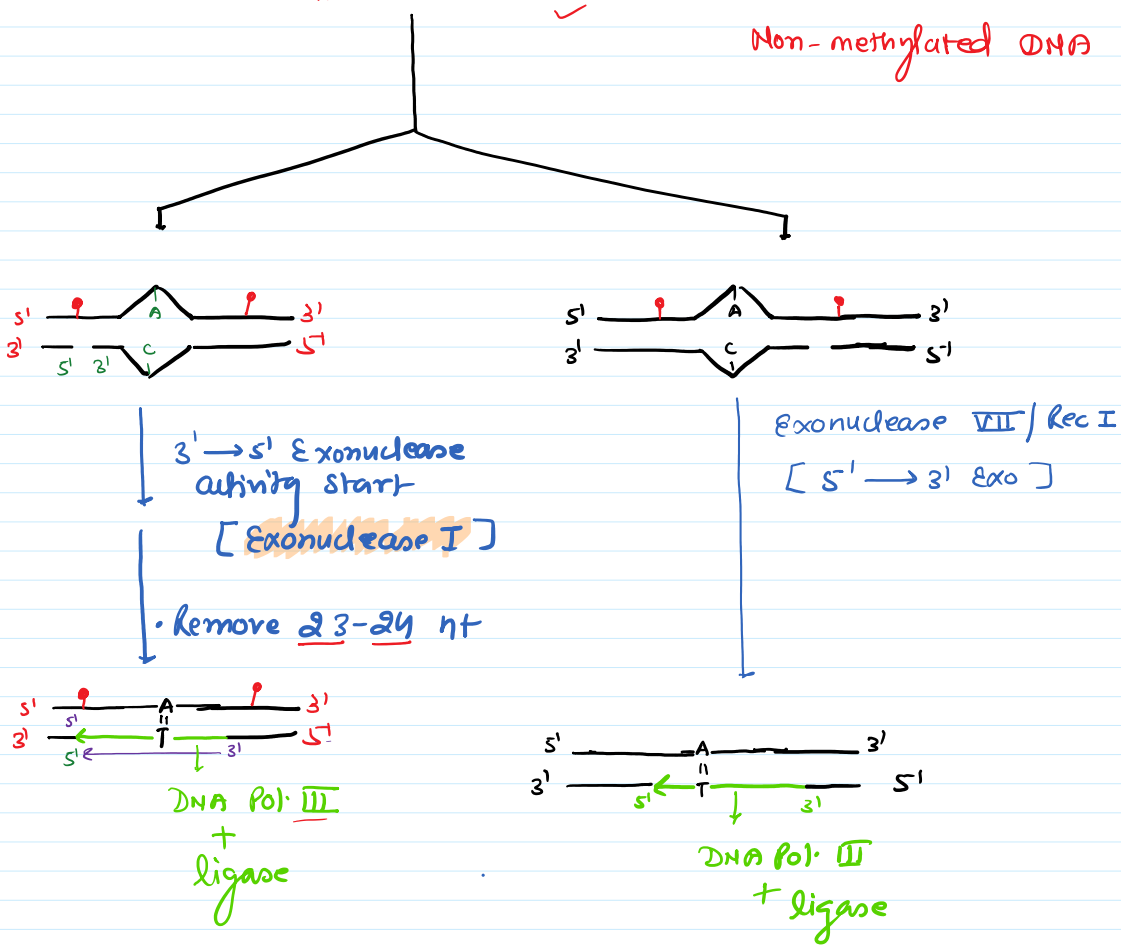
MutS → • Recognize mismatch
• Use ATP
• Induce Bending of DNA

MutL → Trigger Endonuclease activity of MutH

MutH → Endonuclease Activity +nt



• Hemimethylated DNA
↓
MutH induce Cut on Non-methylated DNA



⇒ Mismatch Repair System in Eukaryotes

↳ Replication Coupled Repair

↳ worked in S- Phase of Eukaryotic Cell Cycle

Enzyme -

Mut S Homolog [MSH] → 2 Subunit MSH α & β
↳ mismatch Recognize

Mut L Homolog [MLH] → Contain Endonuclease activity

Mut H Homolog - Nf

- New Strand Can be distinguished by trace of dagging Strand

Gap filling = DNA Pol. δ/ε

DNA ligase = Nick sealing

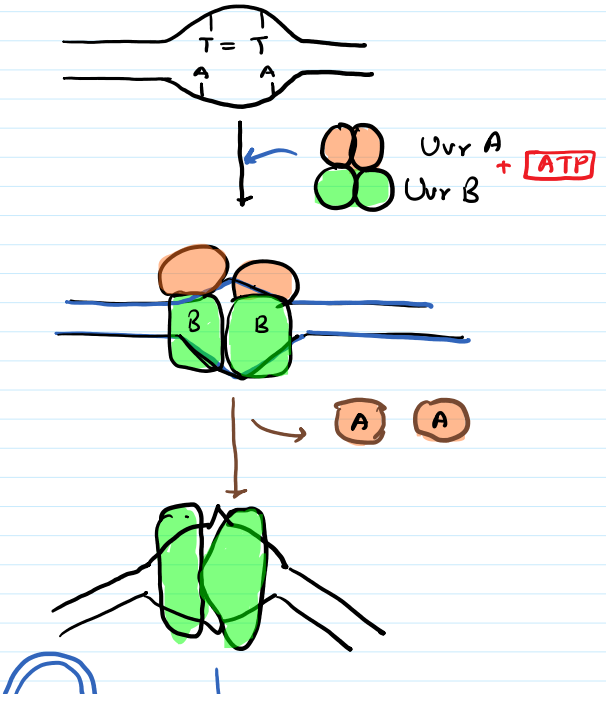
(ii) Nt Excision Repair

- Bulky Damage
- Most active in G1 Phase

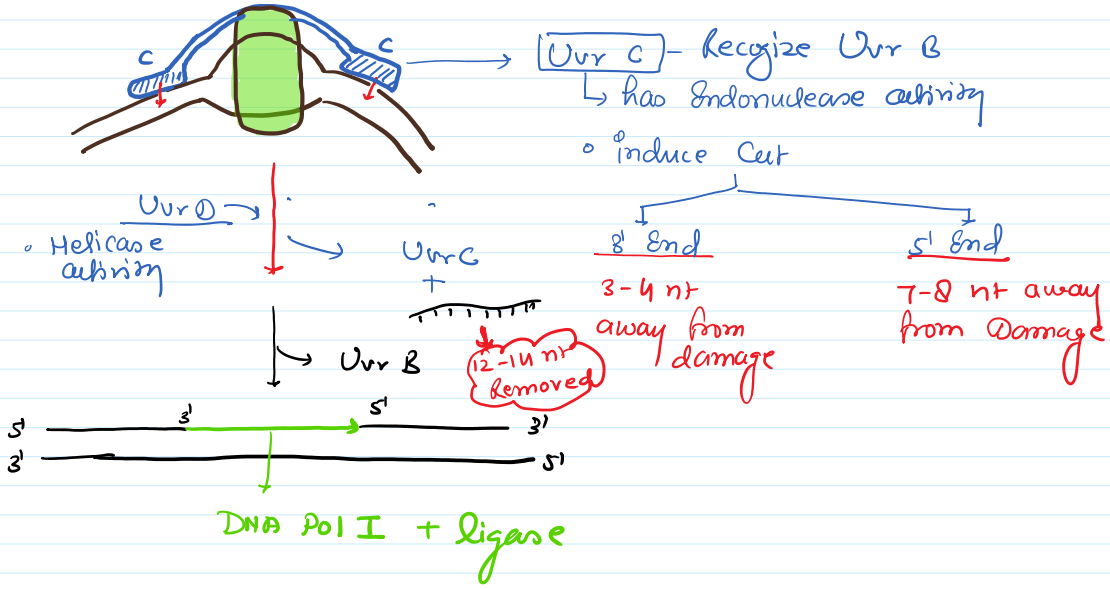
Enzyme

Prokaryote [E.coli]

Uvr A, Uvr B, Uvr C, D, F



Uvr A + Uvr B
+
- Recognize DNA Damage
- Uvr A has ATPase activity
- Uvr B Bond & met the DNA



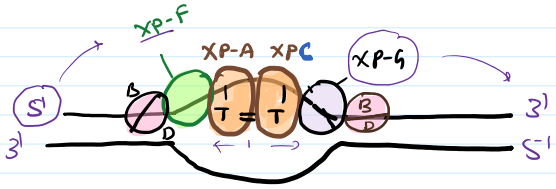
In Eukaryotes

(i) Global Nt Excision Repair
(ii) Transcription Coupled Repair

(1) Global Nt Excision Repair –

Enzymes
XP-A
Xp-B
" - C
" - D
" - E
" - F / ERCC 1
" - G

XP = Xeroderma Pigmentosum
if XP gene → loss of function
↓
leads to Xeroderma Pigmentosum

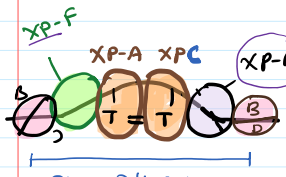


• XP-A & XPC - Recognize Damage
↓
Recruit ∘ XP F toword 5' End of Damage
∘ XPG " 3' " " "

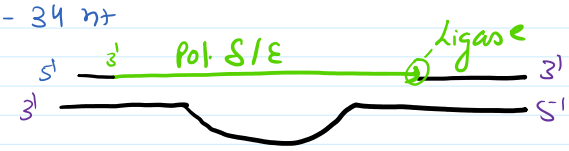
Endonuclease activity
XPF → induce Cut toword 5' End
XPG → " " " 3' End

Endonuclease activity
- XPF → incise cut towards 5' end
- XPG → " " " 3' end

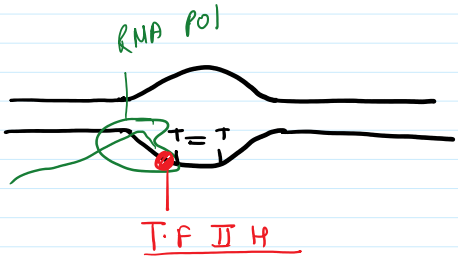
Helicase activity start
[XPB & XPD]



24 - 34 nt



(ii) Transcription Coupled Repair

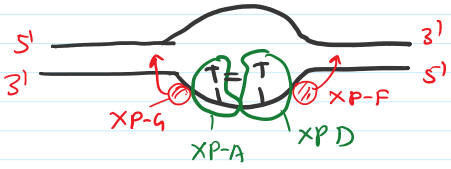


Contain - XP-B - XP D

XP A - XP D
↓
act as helicase

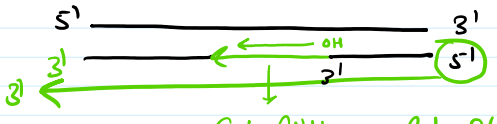
RNA Pol. ←

← Nt Excision Repair System
Recruited by T.F. II H



XP-A & D Recruit XP-G & XPF
↓
induce cut on DNA

XP-A & D Start
Helicase activity

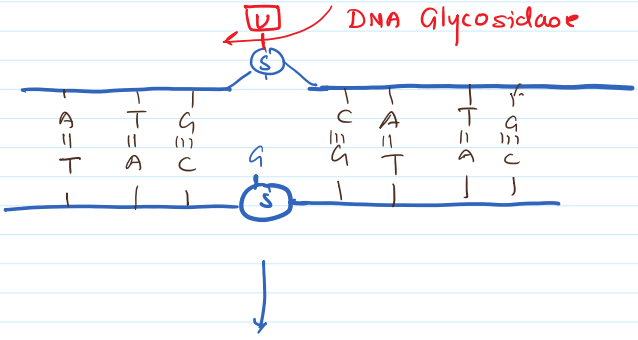


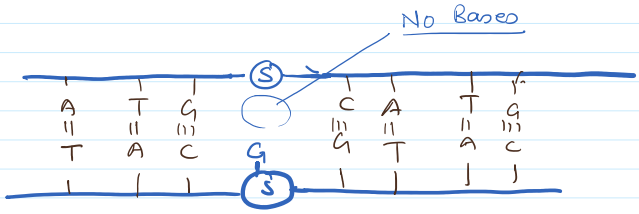
Gap filling Pol δ/ε

Nick Sealing - Ligase

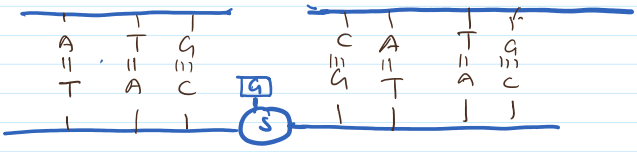
(3) Base Excision Repair

- Single nt mismatch
- mechanism is Conserved in Prokaryote or Eukaryote
- Activate when there is Apurinic site +nt on DNA





AP Endonuclease
- Recognize A.P site
- Break Phosphodiester Bond



Gap is filled by
- DNA Pol. III [Prok.]
- DNA Pol. β [Eukaryote]

Double Strand Break Repair

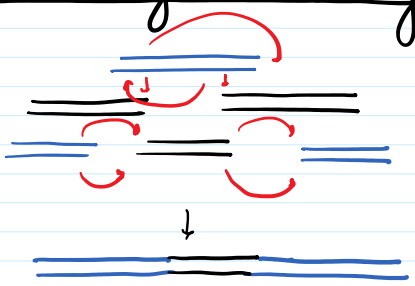
✓ Non-homologus End joining
- Common in Eukaryotes

✓ Homologus Recombination
- common in Prokaryotes
- Lower Eukaryotes

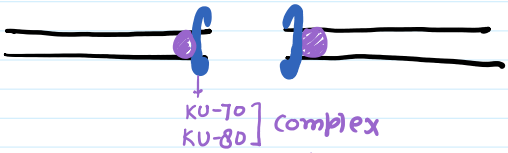
- Common in Eukaryotes
- This is Error Prone mechanism

- Common in Prokaryotes
- lower Eukaryotes
- Dividing Eukaryotes
- Error Proof mechanism

Non Homologus End Joining



mechanism



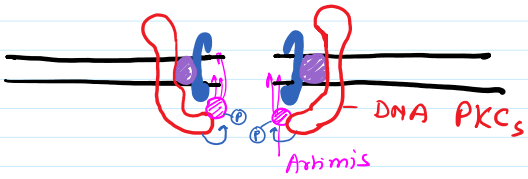
↓

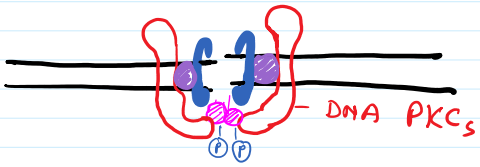
Recruit PKCs

↓

Recruit Artimis

- Endo & Exonuclease
  5'→3'





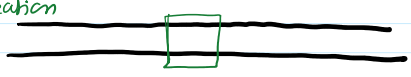
↓ DNA PKCs
↓ Ku-70
↓ Ku-80

DNA Pol. μ
DNA Pol. λ

Also involve in End processing and Polymerization

← ligase IV & XRCC4

→ formation of Phosphodiester Bond



* Double Strand Break Repair

* Double Strand Break Repair

↙ Non-Homologus End Joining [NHEJ]

↘ Homologus Recombination

KU-70] Heterodimer
KU-80]

- DNA PKCs
- Artimis
- Rad 27
- FEN-1 – in Yeast
- WRN

] involve in DNA End Processing

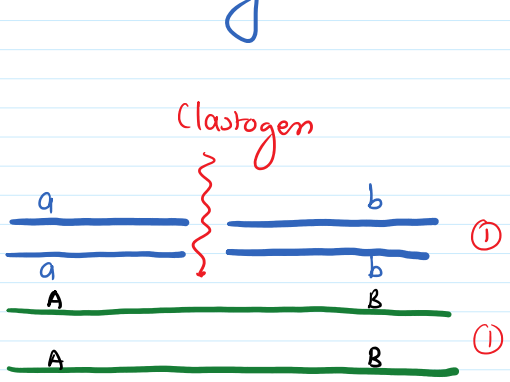
- DNA Pol. μ → Template dependent Pol.
- DNA Pol. λ → Template Independent Pol.

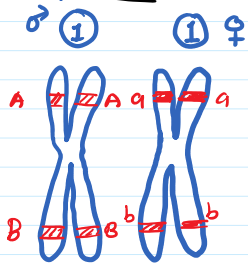
] X-family Polymerase

- Ligase IV & XRCC4

* Homologus Recombination

→ most Common - in meiosis
→ also observed in Ds Break Repair
→ "Most Common Repair Process in Prokaryote
also Can be Seen in Lower Eukaryote
→ mostly occurs in G_2 Phase





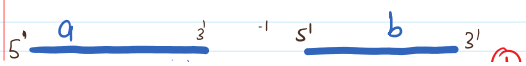
Homologus Chromasome

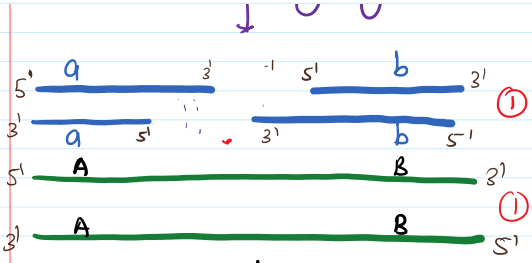
in Bacteria
Rec BCD →

In Eukaryote
← Rad 58, Rad 60, Rad 50
[MRX - yeast]

in meiosis
spo11 – induced Ds Break in Homologus Chromasome

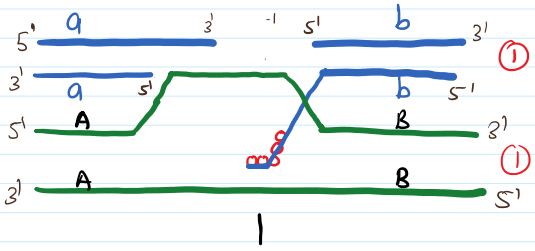
Processing of 5' End

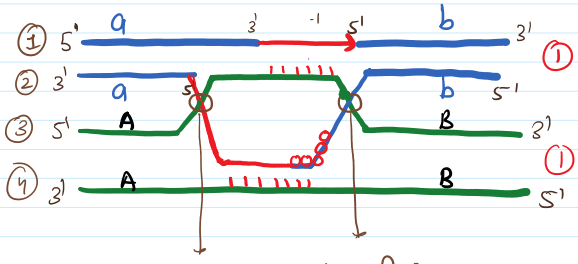




Strand Invasion

Rec A - Prok. Rad 51 - Euk.



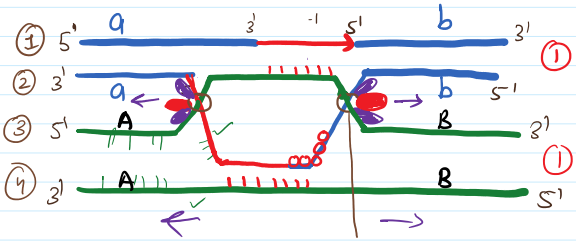


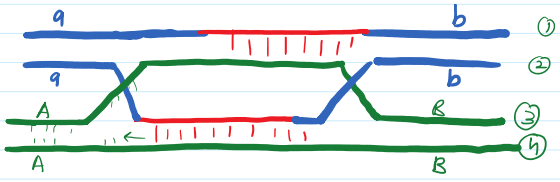
Branch Point [2 Holliday Junction]

Branch Migration

Pro.
RuvA
RuvB

Euk
Not Clear





Resolution

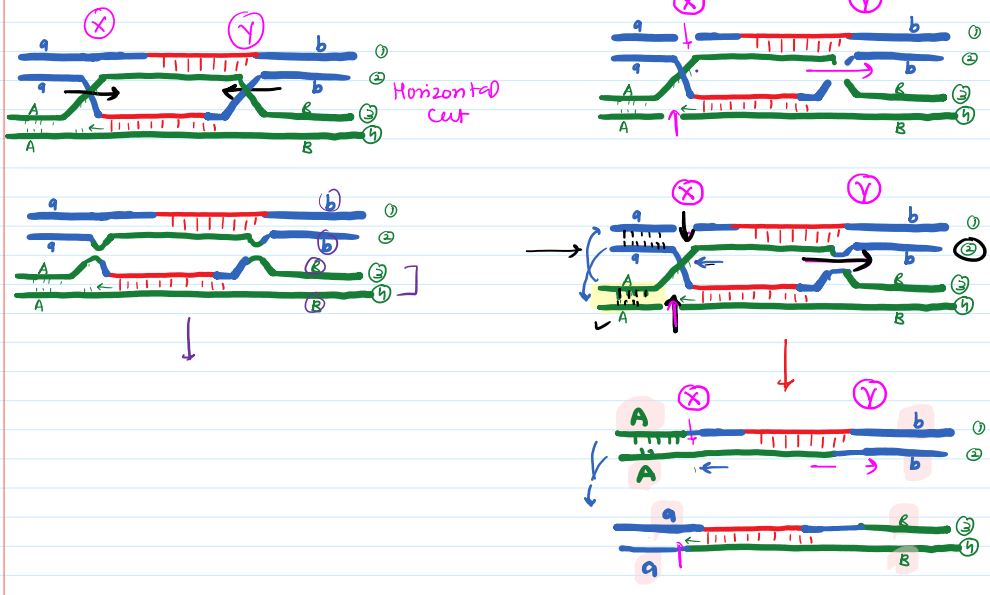
Bacteria

Ruv-C

Euk:

- Rad 51, WRN, XRCC4, BLM

Resolution



Recombination

- when there is 2 Cut on DNA at different Place

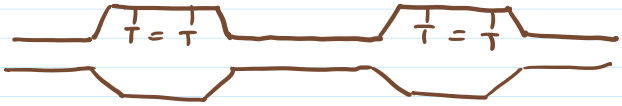
[1 is Horizontal & other is verticle]

Protein involve in Homologus Recombination ⇒

	Bacteria	Eukaryote
① Pairing of Homologous Chromosome & Strand invasion	Rec A	Rad 51, BRCA1
② Processing of Ds DNA	Rec BCD	Rad 50 Rad 58, Rad 60 (mRX - yeast)
③ Branch migration	Ruv AB Complex	———
④ Resolution	Ruv C	Rad 51 XRCC4 / XRCC3 WRN BLM

SOS Repair

- K/a Translesion DNA Synthesis [TLS DNA Synthesis]
- Error prone Repair mechanism



DNA Damage at multiple site

[Excessive DNA Damage]

→ In This Situation Translesion DNA Synthesis start

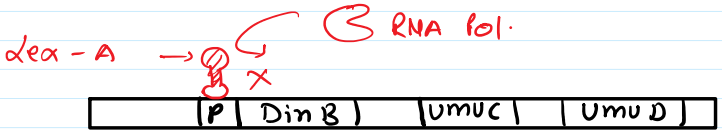
- Enzyme involve in TLS DNA Synthesis has inducible expression
  - DNA Pol. IV & V
- RecA induce Expression of DNA Pol. IV & V

* In Excessive DNA Damage
  - ↳ Rec A Expression ↑↑
  - ↳ involve Homologus Recombination start in

RecA ⊕ → DNA Pol. IV & V

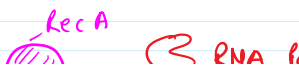
(i) In Normal Condition

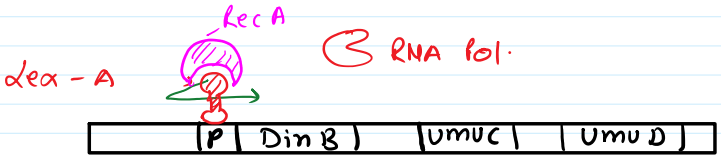
→ DNA Pol. IV & V Expression is Blocked by Lex-A Repressor



(ii) Excessive DNA Damage

* Rec A Expression ↑



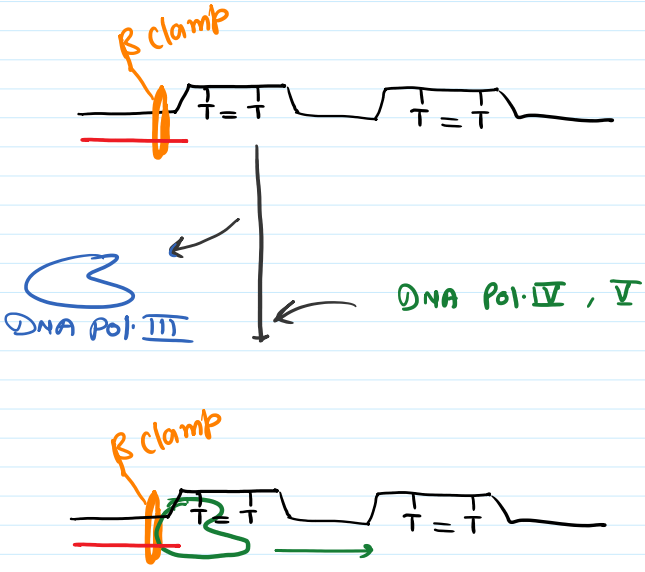


Rec A Activates Autoproteolytic activity of lex-A

Lex - A Removed from Promoter

→ RNA Pol. Start Expression of Din B , umuC & umuD

↓ DNA Pol. IV ; ↓ DNA Pol. V



* In Eukaryotes → TLS Pol.

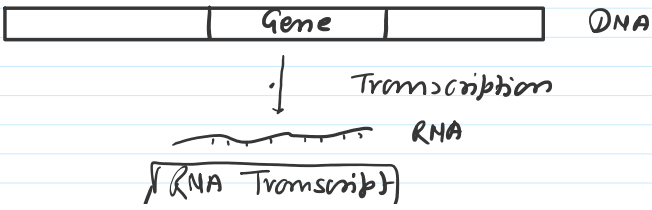
Rev 1 — add any nt.

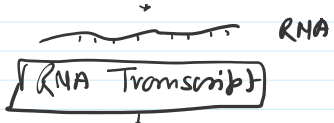
μ → add only adenine

ι → add any nt

] Error prone .

Transcription





Adaptor molecule
- eg - t RNA

Protein Synthesis
m-RNA

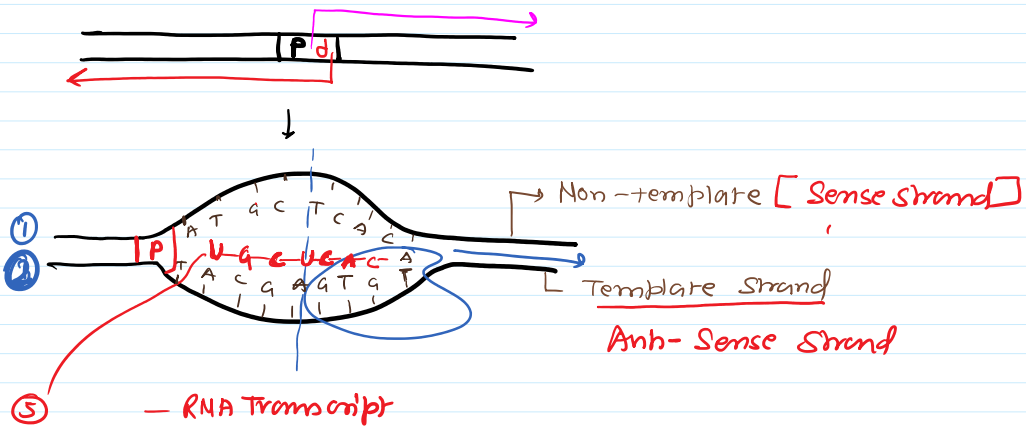
Catalytic Role
- Type I & II intoron
- Ribozyme

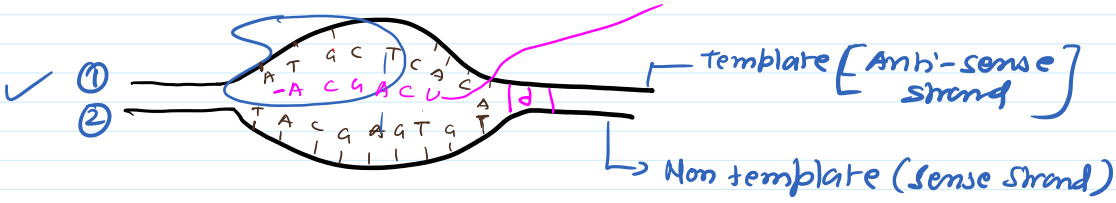
⇒ Types of RNA

hn RNA
m RNA → most Abundant in cytoplasm
t RNA
r RNA → most Abundant in Nucleus
Sc RNA
Sno RNA
mi RNA
Si RNA
Pi RNA
g RNA
} ; RNA

* RNA Transcript Synthesis is always 5' → 3' direction

Orientation of Promoter, determines template and non template strand for RNA Transcript





* Anti-Sense technology is used by this information

eg- flavor-Saver Tomato